

SEQUENCE LISTING

IAP20 Rec'd 16/06/2006
R 2006

SEQ ID 1 – NadA from strain 2996, with C-terminus deletion

MKHFPSKVLTTAILATFCSGALAATNDDDVKAATVAIAAAYNNQEIINGFKAGETIYDIDEDEGTITKKDATAA
 DVEADDFKGLGLKKVVTNLTKTVNENKQNVDAKVAAESEIEKLTTKLADTDAALADTAALDATTNALNKLGE
 5 NITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDIADSDETNTKADEAVKTANEAKQTAEETKQNVDAVK
 AAETAAGKAEEAAGTANTAAADKAEEAVAAKVTDIKADIATNKDNIAKKANSADVYTREESDSKFVRIDGLNATTE
 KLDTRLASAEKSIADHDTRLNLGKTVSDLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed

ATNDDDVKAATVAIAAAYNNQEIINGFKAGETIYDIDEDEGTITKKDATAADVEADDFKGLGLKKVVTNLTKV
 10 NENKQNVDAVKAAESEIEKLTTKLADTDAALADTAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAV
 ADTVDKHAEAFNDIADSDETNTKADEAVKTANEAKQTAEETKQNVDAVKAAETAAGKAEEAAGTANTAAADKA
 EEEAVAAKVTDIKADIATNKDNIAKKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNL
 GKTVDLKRTRQGLAEQAALSGLFQPYNVG

SEQ ID 3 – AG741 from MC58 strain

15 VAADIGAGLADALTAPLDHKDKGLQSLTLQSVRKNEKLKLAQGAEKTYGNQDSLNTGKLKNDKVSRFDFIRQ
 IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDFKLPPEGGRATYRG
 AFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGYSLSLGF
 KAQEVAEKGSAEVKTVNGIRHIGLAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

20 VSAVIGSAAVGAKSAVDRRTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGVYNRHLLLQGVATEG
 EKQFVGQIARSEQAAEGVNYITVASLPTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTVYMGIL
 TPEEQAQITQKVSTTVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDA
 AQYPDIFVSTKFNNGKKLVSDGNLTMHGKTAPEVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDFYL
 VNVMGKTSVRIDIQIEAAKQ

SEQ ID 6 – AG287 from MC58 strain

SPDVKSADTLSKPAAPVSEKETEAKEDAPQAGSQGQGAPSQGSQDMAAVSEENTGNGGAVTADNPKNEDVA
 QNDMPQNAAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQSPANQPDMANAADGMQGDDPSAGGQNAGNTAAQG
 30 ANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDSLNGVLIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEF
 EKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTS FARFRRSARSRRSLPAEMPLIPVNQAD
 TLIVDGEAVSLTGHSGNIFAPEGNRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLFHTENGRP
 YPTRGRFAAKVDFGSKSVDGIIDSGDDLHMGTKFKAAIDGNQFKGTWTENGSGDVSGKFYGPAGEEVAGKSY
 RPTDAEKGFFGVFAGKKEQD

SEQ ID 7 – 287-953 hybrid

MASPDVKSADTLSKPAAPVSEKETEAKEDAPQAGSQGQGAPSQGSQDMAAVSEENTGNGGAAATDKPKNEDE
 GAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAPPDAGESEQSPANQPDMANADGMQGDDPSAGGQNAGNTAA
 QGTNQAENNQTAGSQNPASSTNPSATNSGGDFGRTNVGNSVVIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKS
 EFEKLSDADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTS FARFRRSARSRRSLPAEMPLI
 40 PVNQADTLIVDGEAVSLTGHSGNIFAPEGNRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLFH
 TENGRRPSPSRGRFAAKVDFGSKSVDGIIDSGDLHMGTKFKAAIDGNQFKGTWTENGSGDVSGKFYGPAGEEV
 AGKSYRPTDAEKGFFGVFAGKKEQDGSGGGGATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKR

DGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSDGNLTMHGKTAPVKLKAEK
FNCYQSPMAKTEVCGGDFTTIDRTKWGVVDYLNVGMTKSVRIDIQIEAAKQ*

SEQ ID 8 – 936-741 hybrid

MVSAGIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGVNRHLLLQGVATE
5 GEKQFVGQIARSEQAAEGVNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGI
LTPEEQAQITQKVSTTVGVQKVITLYQNYVQRGSGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN
EKLKLAQGAEKTYNGDSLNTGKLNDKVSRFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDS
EHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNV
DLAAADIKPDGKRHAVISGSVLYNQAEGSYSLGIFGGKAQEVAEVKTVNGIRHIGLAAKQ*

SEQ ID 9 – linker

GSGGGG

SEQ ID 10 – 741 sequence

CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQGAEKTYNGDSLNTGKLNDKVS
RFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGG
15 RATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGSY
SLGIFGGKAQEVAEVKTVNGIRHIGLAAKQ

SEQ ID 11 – 741 sequence

CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQGAEKTYNGDSLNTGKLNDKVS
RFDFIRQIEVDGQLITLESGEFQIYKQDHSAVVALQIEKINNPDKIDSЛИQRSFLVSGLGGEHTAFNQLPDGK
20 AEYHGKAFSSDDAGGKLTYTIDFAAKQGHGKIEHLKTPEQNVELAAELKADEKSHAVILGDTRYGSEEKGTYH
LALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ

SEQ ID 12 – 741 sequence

CSSGGGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEDSIPQNGTLTLSAQGAEKTFKAGDKDNSLNTG
KLNDKISRFDFVQKIEVDGQQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDSLINQRSFLVSGLGGEHTA
25 FNQLPGGKAEHGKAFSSDDPNGLHYSIDFTKKQGYGRIEHLKTLEQNVELAAELKADEKSHAVILGDTRYG
SEEKGTYHLALFGDRAQEIAGSATVKIGEKVHEIGIAGKQ